

GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCCGGTT	GTCCTGGAGC	AGGGGCCAG	60
GAATTCGTGAT	GTGAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCACTCAG	AGAAG ATG AAG GAT	124
I D I G K E Y I I P S P G Y R S V R E R					M K D	3
ATC GAC ATA GGA AAA GAG TAT ATC ATC CCC AGT CCT GGG TAT AGA AGT GTG AGG GAG AGA					R	23
T S T S G T H R D R E D S K F R R T R P					43	184
ACC AGC ACT TCT GGG ACG CAC AGA GAC CGT GAA GAT TCC AAG TTC AGG AGA ACT CGA CCG					63	244
L E C Q D A L E T A A R A E G L S L D A					304	
TTG GAA TGC CAA GAT GCC TTG GAA ACA GCA GCC CGA CGA GCC GAG GGC CTC TCT CTT GAT GCC					83	
S M H S Q L R I L D E E H P K G K Y H H					364	
TCC ATG CAT TCT CAG CTC AGA ATC CTG GAT GAG GAG CAT CCC AAG GGA AAG TAC CAT CAT						
G L S A L K P I R T T S K H Q H P V D N					103	
GGC TTG AGT GCT CTG AAG CCC ATC CGG ACT ACT TCC AAA CAC CAG CAC CCA GTG GAC AAT					424	
A G L F S C M T F S W L S S L A R V A H					123	
GCT GGG CTT TTT TCC TGT ATG ACT TTT TCG TGG CTT TCT TCT CTG GCC CGT GTG GCC CAC					484	
K K G E L S M E D V W S L S K H E S S D					143	
AAG AAG GGG GAG CTC TCA ATG GAA GAC GTG TGG TCT CTG TCC AAG CAC GAG TCT TCT GAC					544	
V N C R R L E R L W Q E E L N E V G P D					163	
GTG AAC TGC AGA AGA CTA GAG AGA CTG TGG CAA GAA GAG CTG AAT GAA GTT GGG CCA GAC					604	
A A S L R R V V W I F C R T R L I L S I					183	
GCT GCT TCC CTG CGA AGG GTT GTG TGG ATC TTC TGC CGC ACC AGG CTC ATC CTG TCC ATC					664	
V C L M I T Q L A G F S G P A F M V K H					203	
GTG TGC CTG ATG ATC ACG CAG CTG GCT GGC TTC AGT GGA CCA GCC TTC ATG GTG AAA CAC					724	

FIGURE 1A

L	L	E	Y	T	Q	A	T	E	S	N	L	Q	Y	S	L	L	L	V	L	223
CTC	TTG	GAG	TAT	ACC	CAG	GCA	ACA	GAG	TCT	AAC	CTG	CAG	TAC	AGC	TTG	TTG	TTA	GTG	CTG	784
G	L	L	L	T	E	I	V	R	S	W	S	L	A	L	T	W	A	L	N	243
GGC	CTC	CTC	CTG	ACG	GAA	ATC	GTG	CGG	TCT	TGG	TCG	CTT	GCA	CTG	ACT	TGG	GCA	TTG	AAT	844
Y	R	T	G	V	R	L	R	G	A	I	L	T	M	A	F	K	K	I	L	263
TAC	CGA	ACC	GGT	GTC	CGC	TTG	CGG	GGG	GCC	ATC	CTA	ACC	ATG	GCA	TTT	AAG	AAG	ATC	CTT	904
K	L	K	N	I	K	E	K	S	L	G	E	L	I	N	I	C	S	N	D	283
AAG	TTA	AAG	AAC	ATT	AAA	GAG	AAA	TCC	CTG	GGT	GAG	CTC	ATC	AAC	ATT	TGC	TCC	AAC	GAT	964
G	Q	R	M	F	E	A	A	A	V	G	S	L	L	A	G	G	P	V	V	303
GGG	CAG	AGA	ATG	TTT	GAG	GCA	GCA	GCC	GTT	GGC	AGC	CTG	CTG	GCT	GGA	GGA	GGA	CCC	GTT	1024
A	I	L	G	M	I	Y	N	V	I	I	L	G	P	T	G	F	L	G	S	323
GCC	ATC	TTA	GGC	ATG	ATT	TAT	AAT	GTA	ATT	ATT	CTG	GGA	CCA	ACA	GGC	TTC	CTG	GGA	TCA	1084
A	V	F	I	L	F	Y	P	A	M	M	F	A	S	R	L	T	A	Y	F	343
GCT	GTT	TTT	ATC	CTC	TTT	TAC	CCA	GCA	ATG	ATG	TTT	GCA	TCA	CGG	CTC	ACA	GCA	TAT	TTC	1144
R	R	K	C	V	A	A	T	D	E	R	V	Q	K	M	N	E	V	L	T	363
AGG	AGA	AAA	TGC	GTG	GCC	GCC	ACG	GAT	GAA	CGT	GTC	CAG	AAG	ATG	AAT	GAA	GTT	CTT	ACT	1204
Y	I	K	F	I	K	M	Y	A	W	V	K	A	F	S	Q	S	V	Q	K	383
TAC	ATT	AAA	TTT	ATC	AAA	ATG	TAT	GCC	TGG	GTC	AAA	GCA	TTT	TCT	CAG	AGT	GTT	CAG	AAA	1264
I	R	E	E	R	R	I	L	E	K	A	G	Y	F	Q	S	I	T	V	403	
ATC	CGC	GAG	GAG	GAG	CGT	CGG	ATA	TTG	GAA	AAA	GCC	GGG	TAC	TTC	CAG	AGC	ATC	ACT	GTG	1324
G	V	A	P	I	V	V	V	I	A	S	V	V	T	F	S	V	H	M	T	423
GGT	GTG	GCT	CCC	ATT	GTG	GTG	GTG	ATT	GCC	AGC	GTG	GTG	ACC	TTC	TCT	GTT	CAT	ATG	ACC	1384

FIGURE 1B

L	G	F	D	L	T	A	A	Q	A	F	T	V	V	T	V	F	N	S	M	443	
CTG	GGC	TTC	GAT	CTG	ACA	GCA	GCA	CAG	GCT	TTC	ACA	GTG	GTG	ACA	GTC	TTC	AAT	TCC	ATG	1444	
T	F	A	L	K	V	T	P	F	S	V	K	S	L	S	E	A	S	V	A	463	
ACT	TTT	GCT	TTG	AAA	GTA	ACA	CCG	TTT	TCA	GTA	AAG	TCC	CTC	TCA	GAA	GCC	TCA	GTG	GCT	1504	
V	D	R	F	K	S	L	F	L	M	E	E	V	H	M	I	K	N	K	P	483	
GTT	GAC	AGA	TTT	AAG	AGT	TTG	TTT	CTA	ATG	GAA	GAG	GTG	CAC	ATG	ATA	AAG	AAC	AAA	CCA	1564	
A	S	P	H	I	K	I	E	M	K	N	A	T	L	A	W	D	S	S	H	503	
GCC	AGT	CCT	CAC	ATC	AAG	ATA	GAG	ATG	AAA	AAT	GCC	ACC	TTG	GCA	TGG	GAC	TCC	TCC	CAC	1624	
S	S	I	Q	N	S	P	K	L	T	P	K	M	K	K	D	K	R	A	S	523	
TCC	AGT	ATC	CAG	AAC	TCG	CCC	AAG	CTG	ACC	CCC	AAA	ATG	AAA	AAC	GAC	AAG	AGG	GCT	TCC	1684	
R	G	K	K	E	K	V	R	Q	I	Q	R	T	E	H	Q	A	V	L	A	543	
AGG	GGC	AAG	AAA	GAG	AAG	GTG	AGG	CAG	CTG	CAG	CGC	ACT	GAG	CAT	CAG	GCG	GCG	GTG	CTG	GCA	1744
E	Q	K	G	H	L	L	D	S	D	E	R	P	S	P	E	E	E	E	563		
GAG	CAG	AAA	GGC	CAC	CTC	CTC	CTG	GAC	AGT	GAC	GAG	CGG	CCC	AGT	CCC	GAA	GAG	GAA	GAA	1804	
G	K	H	I	H	L	G	H	L	R	L	Q	R	T	L	H	S	I	D	L	583	
GGC	AAG	CAC	ATC	CAC	CTG	GGC	CAC	CTG	CGC	TTA	CAG	AGG	ACA	CTG	CAC	AGC	ATC	GAT	CTG	1864	
E	I	Q	E	G	K	L	V	G	I	C	G	S	V	G	S	G	K	T	S	603	
GAG	ATC	CAA	GAG	GGT	AAA	CTG	GTG	GGA	ATC	TGC	GGC	AGT	GTG	GGA	AGT	GGA	AAA	ACC	TCT	1924	
L	I	S	A	I	L	G	Q	M	T	L	E	G	S	I	A	I	S	G	623		
CTC	ATT	TCA	GCC	ATT	TTA	GGC	CAG	ATG	ACG	CTT	CTA	GAG	GGC	AGC	ATT	GCA	ATC	AGT	GGA	1984	
T	F	A	Y	V	A	Q	Q	A	W	I	L	N	A	T	L	R	D	N	I	643	
ACC	TTC	GCT	TAT	GTG	GCC	CAG	CAG	GCC	TGG	ATC	CTC	AAT	GCT	ACT	CTG	AGA	GAC	AAC	ATC	2044	

L	F	G	K	E	Y	D	E	R	Y	N	S	V	L	N	S	C	C	L	663	
CTG	TTT	GGG	AAG	GAA	TAT	GAT	GAA	GAA	AGA	TAC	AAC	TCT	GTG	CTG	AAC	AGC	TGC	TGC	2104	
R	P	D	L	A	I	L	P	S	S	D	L	T	E	I	G	E	R	G	683	
AGG	CCT	GAC	CTG	GCC	ATT	CTT	CCC	AGC	AGC	GAC	CTG	ACG	GAG	ATT	GGA	GAG	CGA	GGA	2164	
N	L	S	G	G	Q	R	Q	R	I	S	L	A	R	A	L	Y	S	D	R	703
AAC	CTG	AGC	GGT	GGG	CAG	CGC	CAG	AGG	ATC	AGC	CTR	GCC	CGG	GCC	TTG	TAT	AGT	GAC	AGG	2224
S	I	Y	I	L	D	D	P	L	S	A	L	D	A	H	V	G	N	H	I	723
AGC	ATC	TAC	ATC	CTG	GAC	GAC	CCC	CTC	AGT	GCC	TTA	GAT	GCC	CAT	GTG	GGC	AAC	CAC	ATC	2284
F	N	S	A	I	R	K	H	L	K	S	K	T	V	L	F	V	T	H	Q	743
TTC	AAT	AGT	GCT	ATC	CGG	AAA	CAT	CTC	AAG	TCC	AAG	ACA	GTT	CTG	TTT	GTT	ACC	CAC	CAG	2344
L	Q	Y	L	V	D	C	D	E	V	I	F	M	K	E	G	C	I	T	E	763
TTA	CAG	TAC	CTG	GTT	GAC	TGT	GAT	GAA	GTG	ATC	TTC	ATG	AAA	GAG	GGC	TGT	ATT	ACG	GAA	2404
R	G	T	H	E	E	L	M	N	L	N	G	D	Y	A	T	I	F	N	N	783
AGA	GGC	ACC	CAT	GAG	GAA	CTG	ATG	AAT	TTA	AAT	GGT	GAC	TAT	GCT	ACC	ATT	TTT	AAT	AAC	2464
L	L	L	G	E	T	P	P	V	E	I	N	S	K	K	E	T	S	G	S	803
CTG	TTG	CTG	GGA	GAG	ACA	CCG	CCA	GTT	GAG	ATC	AAT	TCA	AAA	AAG	GAA	ACC	AGT	GGT	TCA	2524
Q	K	K	S	Q	D	K	G	P	K	T	G	S	I	K	K	E	K	A	V	823
CAG	AAG	AAG	TCA	CAA	GAC	AAG	GGT	CCT	AAA	ACA	GGA	TCA	ATA	AAG	AAG	GAA	AAA	GCA	GTA	2584
K	P	E	E	Q	L	V	Q	L	E	E	K	G	Q	G	S	V	P	W	843	
AAG	CCA	GAG	GAA	GGG	CAG	CTT	GTG	CAG	CTG	GAA	GAG	AAA	GGG	CAG	GGT	TCA	GTG	CCC	TGG	2644
S	V	Y	G	V	Y	I	Q	A	A	G	G	P	L	A	F	L	V	I	M	863
TCA	GTA	TAT	GGT	GTC	TAC	ATC	CAG	GCT	GCT	GGG	GGC	CCC	TTG	GCA	TTC	CTG	GTT	ATT	ATG	2704
A	L	F	M	L	N	V	G	S	T	A	F	S	T	W	W	L	S	Y	W	883
GCC	CTT	TTC	ATG	CTG	AAT	GTA	GGC	AGC	ACC	GCC	TTC	AGC	ACC	TGG	TGG	TTG	AGT	TAC	TGG	2764

I	K	Q	G	S	G	N	T	T	V	T	R	G	N	E	T	S	V	S	D	903
ATC	AAG	CAA	GGA	AGC	GGG	AAC	ACC	ACT	GTG	ACT	CGA	GGG	AAC	GAG	ACC	TCG	GTG	AGT	GAC	2884
S	M	K	D	N	P	H	M	Q	Y	Y	A	S	I	Y	A	L	S	M	A	923
AGC	ATG	AAG	GAC	AAT	CCT	CAT	ATG	CAG	TAC	TAT	GCC	AGC	ATC	TAC	GCC	CTC	TCC	ATG	GCA	2884
V	M	L	I	L	K	A	I	R	G	V	V	F	V	K	G	T	L	R	A	943
GTC	ATG	CTG	ATC	CTG	AAA	GCC	ATT	CGA	GGG	GTG	GTC	TTT	GTC	AAG	GGC	ACG	CTG	CGA	GCT	2944
S	S	R	L	H	D	E	L	F	R	R	I	L	R	S	P	M	K	F	F	963
TCC	TCC	CGG	CTG	CAT	GAC	GAG	CTT	TTC	CGA	AGG	ATC	CTT	CGA	AGC	CCT	ATG	AAG	TTT	TTT	3004
D	T	T	P	T	G	R	I	L	N	R	F	S	K	D	M	D	E	V	D	983
GAC	ACG	ACC	CCC	ACA	GGG	AGG	ATT	CTC	AAC	AGG	TTT	TCC	AAA	GAC	ATG	GAT	GAA	GTT	GAC	3064
V	R	L	P	F	Q	A	E	M	F	I	Q	N	V	I	L	V	F	F	C	1003
GTG	CGG	CTG	CCG	TTC	CAG	GCC	GAG	ATG	TTC	ATC	CAG	AAC	GTT	ATC	CTG	GTG	TTC	TTC	TGT	3124
V	G	M	I	A	G	V	F	P	W	F	L	V	A	V	G	P	L	V	I	1023
GTG	GCA	ATG	ATC	GCA	GGA	GTC	TTC	CCG	TGG	TTC	CTT	GTG	GCA	GTG	GGG	CCC	CTT	GTC	ATC	3184
L	F	S	V	L	H	I	V	S	R	V	L	I	R	E	L	K	R	L	D	1043
CTC	TTT	TCA	GTC	CTG	CAC	ATT	GTC	TCC	AGG	GTC	CTG	ATT	CGG	GAG	CTG	AAG	CGT	CTG	GAC	3244
N	I	T	Q	S	P	F	L	S	H	I	T	S	S	I	Q	G	I	A	T	1063
AT	ATC	ACG	CAG	TCA	CCT	TTC	CTC	TCC	CAC	ATC	ACG	TCC	AGC	ATA	CAG	GGC	CTT	GCC	ACC	3304
I	H	A	Y	N	K	G	Q	E	F	L	H	R	Y	Q	E	L	I	D	D	1083
ATC	CAC	GCC	TAC	AAT	AAA	GGG	CAG	GAG	TTT	CTG	CAC	AGA	TAC	CAG	GAG	CTG	CTG	GAT	GAC	3364
N	Q	A	P	F	F	L	F	T	C	A	M	R	W	L	A	V	R	L	D	1103
AAC	CAA	GCT	CCT	TTT	TTT	TTG	TTT	ACG	TGT	GGC	ATG	CGG	TGG	CTG	GCT	GTG	CGG	CTG	GAC	3424

L	I	S	I	A	L	I	T	T	G	L	M	I	V	L	M	H	G	Q	1123	
CTC	ATC	AGC	ATC	GCC	CTC	ATC	ACC	ACC	ACG	GGG	CTG	ATG	ATC	GTT	CTT	ATG	CAC	GGG	CAG	3484
I	P	P	A	Y	A	G	L	A	I	S	Y	A	V	Q	L	T	G	L	F	1143
ATT	CCC	CCA	GCC	TAT	GCG	GGT	CTC	GCC	ATC	TCT	TAT	GCT	GTC	CAG	RTA	ACG	GGG	CTG	TTC	3544
Q	F	T	V	R	L	A	S	E	T	E	A	R	F	T	S	V	E	R	I	1163
CAG	TTT	ACG	GTC	AGA	CTG	GCA	TCT	GAG	ACA	GAA	GCT	CGA	TTC	ACC	TCG	GTG	GAG	AGG	ATC	3604
N	H	Y	I	K	T	L	S	L	E	A	P	A	R	I	K	N	K	A	P	1183
AAT	CAC	TAC	ATT	AAG	ACT	CTG	TCC	TTG	GAA	GCA	CCT	GCC	AGA	ATT	AAG	AAC	AAG	GCT	CCC	3664
S	P	D	W	P	Q	E	G	E	V	T	F	E	N	A	E	M	R	Y	R	1203
TCC	CCT	GAC	TGG	CCC	CAG	GAG	GGA	GAG	GTG	ACC	TTT	GAG	AAC	GCA	GAG	ATG	AGG	TAC	CGA	3724
E	N	L	P	L	V	L	K	K	V	S	F	T	I	K	P	K	E	K	I	1223
GAA	AAC	CTC	CCT	CTC	GTC	CTA	AAG	AAA	GTA	TCC	TTC	ACG	ATC	AAA	CCT	AAA	GAG	AAG	ATT	3784
G	I	V	G	R	T	'G	S	G	K	S	S	L	G	M	A	L	F	R	L	1243
GGC	ATT	GTG	GGG	CGG	ACA	GGA	TCA	GGG	AAG	TCC	TCG	CTG	GGG	ATG	GCC	CTC	TTC	CGT	CTG	3844
V	E	L	S	G	C	I	K	I	D	G	V	R	I	S	D	I	G	L	1263	
GTG	GAG	TTA	TCT	GGA	GGC	TGC	ATC	AAG	ATT	GAT	GGA	GTG	AGA	ATC	AGT	GAT	ATT	GGC	CTT	3904
A	D	L	R	S	K	L	S	I	I	P	Q	E	P	V	L	F	S	G	T	1283
GCC	GAC	CTC	CGA	AGC	AAA	CTC	TCT	ATC	ATT	CCT	CAA	GAG	CCG	GTG	CTG	TTC	AGT	GGC	ACT	3964
V	R	S	N	L	D	P	F	N	Q	Y	T	E	D	Q	I	W	D	A	L	1303
GTC	AGA	TCA	AAT	TTG	GAC	CCC	TTG	AAC	CAG	TAC	ACT	GAA	GAC	CAG	ATT	TGG	GAT	GCC	CTG	4024
E	R	T	H	M	K	E	C	I	A	Q	L	P	L	K	L	E	S	E	V	1323
GAG	AGG	ACA	CAC	ATG	AAA	GAA	TGT	ATT	GCT	CAG	CTA	CCT	CTG	AAA	CTT	GAA	TCT	GAA	GTG	4084

M	E	N	G	D	N	F	S	V	G	E	R	Q	L	I	C	I	A	R	A	1343
ATG	GAG	AAT	GGG	GAT	AAC	TTC	TCA	GTG	GGG	GAA	CGG	CAG	CTC	TTG	TGC	ATA	GCT	AGA	GCC	4144
L	L	R	H	C	K	I	L	I	L	D	E	A	T	A	A	M	D	T	E	1363
CTG	CTC	CGC	CAC	TGT	AAG	ATT	CTG	ATT	TTA	GAT	GAA	GCC	ACA	GCT	GCC	ATG	GAC	ACA	GAG	4204
T	D	L	L	I	Q	E	T	I	R	E	A	F	A	D	C	T	M	L	T	1383
ACA	GAC	TTA	TG	ATT	CAA	GAG	ACC	ATC	CGA	GAA	GCA	TTT	GCA	GAC	TGT	ACC	ATG	CTG	ACC	4264
I	A	H	R	L	H	T	V	L	G	S	D	R	I	M	V	L	A	Q	G	1403
ATT	GCC	CAT	CGC	CTG	CAC	ACG	GTT	CTA	GGC	TCC	GAT	AGG	ATT	ATG	GTG	CTG	GCC	CAG	GGA	4324
Q	V	V	E	F	D	T	P	S	V	L	L	S	N	D	S	S	R	F	Y	1423
CAG	GTG	GTG	GAG	TTT	GAC	ACC	CCA	TCG	GTC	CTR	CTG	TCC	AAC	GAC	AGT	TCC	CGA	TTC	TAT	4384
A	M	F	A	A	E	N	K	V	A	V	K	G	*							1437
GCC	ATG	TTT	GCT	GCT	GCA	GAG	AAC	AAG	GTC	GTC	GTC	AAG	GGC	TGA						4429
CTCCTCCCTGTGACGAAAGTCTCTTTCTTAGAGCATGCCMYKGMMTKCCTGGGGCGGGCCCTTCATCGCGTCCTC																				4508
CTACCGAAACCTGCCTTCTCGATTTCTCGCACAGCAGTTCCGGATTGGCTTGTGTGTTCACTTTAGGGAG																				4587
AGTCATATTTGATTATTGATTATTCCATATTCAATGAAACAAATTAGTTTGTCTTAATTGCACCTAAAG																				4666
GTTCAGGGAACCGTTATTATAATTGATCAGAGGCCTATAATGAGCTTATACGTGTAGCTATATATAATT																				4745
TGTACATAGCCTATATTACAGTGAAATGTAAGCTGTATTATATAAGCACTGTGCTAAAAAA																				4824
AAAAAAAAAGGGGGCCGC																				4847

ALIGN calculates a global alignment of two sequences  
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)  
> SwissProt P33527 - MULTIDRUG RESISTANCE-ASSOCIA 1531 aa vs.  
> MRP-H 1437 aa  
scoring matrix: pam120.mat, gap penalties: -12/-4  
30.9% identity; Global alignment score: 1214

10 20 30 40 50 60  
inputs MALRGPCSADGSDPLWDWNVTWNNTSNPDKFCQNTVLUWVPCFYLWACFPFYFLYLSRH

inputs DRGYIQMTPLNKTKTALGFLLWIVCWADLFYSFWERSRGIFLAPVFLVSPTELLGTTLLA

130	140	150	160	170
inputs TFLIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALK-E-DAQVDLFRDITFYVVF				
	:	:	:	:
	-----MKDIDIGKEYIIPSPGYRSVRERTST-----			
	10	20		

180	190	200	210	220	230
inputs	SLLIQLVLSCFSDRSPLFSETIHDPNPCPES-SASFSLSRITFWWITGLIVRG-YRQPLE				
:	:	:	:	:	:
SGTHRDREDSKFRRTRPLECQDALETAARAEGLSLDASMSQLRILDEEHPKGKYHHGLS					
30	40	50	60	70	80
240	250	260	270	280	290
inputs	G-SDLWSLNKEDTSEQVVPVLV-KNWKKECAKTRKQPVKVVYSSKDP-AQPK-ESSKVDA				
:	:	:	:	:	:
ALKPIRTTCKHQHPVLDINAGLFSCTMF	SWLSS	ALARVAHKKGELS	MEDVWSLSKHESSDVNC		
90	100	110	120	130	140

410	420	430	440	450	460
inputs	LVITNSARKSSTVGEIVNLMCSVDAQRFMDLATYINMIWSAPLQVILALYLLWLNLGPSVL				
: .	: . . . . .	: . . . . .	: . . . . .	: . . . . .	: . . . . .
LKLKN--I	KEKSLGELINICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNYVIIILGPTGF				
270	280	290	300	310	320

FIGURE 2A

## FIGURE 2B

inputs DDPIVNGTQ---EHTKVRSLVYGALGISQGIAVFGYSMAV---SIGGIL----AS  
 :  
 KQGSGNTTVTRGNETSVDSDMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRAS  
 890 900 910 920 930 940  
 1050 1060 1070 1080 1090 1100  
 inputs RCLHVDLLHSILRSPMSFFERTPSGNLVNRPSKELDTVDMSMPEVIKMFMSGSLFNVIGAC  
 :  
 SRLHDELFRRYLRSRPMKPPDTPTGRILNRFSKIMDEVDVRLPFQAEMFIQNVLVFC  
 950 960 970 980 990 1000  
 1110 1120 1130 1140 1150 1160  
 inputs IVILLAT-PIAAIIIPPLGLIYFFVQRFYVASSRQLKRLESVSRSPVYSHPNETLLGVSV  
 :  
 VGMIAVGFPFWFLVAVGPLVILPSVLHIVSRVLIRELKRLUNITQSPFLSHITSSIQGLAT  
 1010 1020 1030 1040 1050 1060  
 1170 1180 1190 1200 1210 1220  
 inputs IRAFEEQERFIHQSDLKVDENQKAYYPSIVANRWLAVRLECVGNICIVLFAALFAVISRHS  
 :  
 IHAYNKGQEFHLRYQELLDINQAPFFLFTCAMRWLAVRLLDLSIALITTTGLMIVLMHGQ  
 1070 1080 1090 1100 1110 1120  
 1230 1240 1250 1260 1270 1280  
 inputs LSAGLVGLSVSYSLQVPTYLNWLVRSSEMETNIVAVERLKEYSETEK-EAPWQIQTAP  
 :  
 IPPAYAGLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAP  
 1130 1140 1150 1160 1170 1180  
 1290 1300 1310 1320 1330 1340  
 inputs PSSWPQVGRVEFRNYCLRYREDLDFVLRHINVTINGGEKVGIVGRTGAGKSSLTLGLFRI  
 :  
 SPDWPQEGERVTPENAEMLRYRENPLVKKVSFTIKPKKEKIGIVGRTGSGKSSLGMALFRL  
 1190 1200 1210 1220 1230 1240  
 1350 1360 1370 1380 1390 1400  
 inputs NESAEGEIIDGINIAKIGLHDLRFKITIIPQDPFVLESGSLRMNLDPFSQYSDEEVWTS  
 :  
 VELSGGCIIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDAL  
 1250 1260 1270 1280 1290 1300  
 1410 1420 1430 1440 1450 1460  
 inputs ELAHLKDFVSAALPDKLDHECAEGGENLSVGQRQLVCLARALLRKTKILVLDDEATAAVDLE  
 :  
 ERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTE  
 1310 1320 1330 1340 1350 1360  
 1470 1480 1490 1500 1510 1520  
 inputs TDDLIQSTIRTOFEDCTVLTIAHRLNTIMDYTRVIVLDKGEIQEYGAPSDLL-QQRGLFY  
 :  
 TDLLIQETIREAFADCTMLTIAHRLHTVLSDRIMVLAQGQVVEFDTPSVLLSNDSSRFY  
 1370 1380 1390 1400 1410 1420  
 1530  
 inputs SM-AKDAGLV----  
 : : : : :  
 AMFAAAENKVAVKG  
 1430

FIGURE 2C